



# A New Record of *Thaxterogaster* Subgenus *Scauri* (Agaricales) from India

Arunima Bose <sup>a</sup>, Arvind Parihar <sup>b</sup>, Alfredo Vizzini <sup>c</sup>  
and Kanad Das <sup>a\*</sup>

<sup>a</sup> Central National Herbarium, Botanical Survey of India, Howrah, West Bengal, 711103, India.

<sup>b</sup> Arunachal Pradesh Regional Centre Botanical Survey of India, Sankie View Post Box No. - 127, Itanagar, 791111, India.

<sup>c</sup> Department of Life Sciences and Systems Biology, University of Torino, 10125 Torino, Italy.

## Authors' contributions

This work was carried out in collaboration among all authors. Author AB designed the study and wrote the first draft of the manuscript. Author AP undertook the survey tour, collected the specimens, and checked the manuscript. Authors AV and KD managed the analyses of the study and revised the manuscript. All authors read and approved the final manuscript.

## Article Information

DOI: <https://doi.org/10.9734/ijpss/2025/v37i45393>

## Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://pr.sdiarticle5.com/review-history/134018>

Original Research Article

Received: 05/02/2025

Accepted: 07/04/2025

Published: 10/04/2025

## ABSTRACT

The present study from Arunachal Pradesh, India, introduces a new record of the genus *Thaxterogaster*, specifically *T. pallidopurpurascens*, a species recently described from China. This study is supported by both morphological and molecular evidence. The species was discovered in temperate to subalpine coniferous forests of the Himalayas. The study provides detailed macro- and micromorphological characteristics, illustrations of the specimen, and molecular phylogenetic analysis.

\*Corresponding author: E-mail: [daskanadbsi@gmail.com](mailto:daskanadbsi@gmail.com);

**Cite as:** Bose, Arunima, Arvind Parihar, Alfredo Vizzini, and Kanad Das. 2025. "A New Record of *Thaxterogaster* Subgenus *Scauri* (Agaricales) from India". *International Journal of Plant & Soil Science* 37 (4):118-28. <https://doi.org/10.9734/ijpss/2025/v37i45393>.

**Keywords:** Agaricales; Basidiomycota; macrofungi; morphology; phylogenetic inferences.

## 1. INTRODUCTION

The family Cortinariaceae R. Heim ex Pouzar em. Niskanen & Liimat. belongs to the suborder Agaricineae Fr. and the order Agaricales Underw. (Basidiomycota R.T. Moore) (Bose et al., 2024a). This is one of the largest families in Basidiomycota, with over 3,157 accepted species and several undescribed species (Soop et al., 2019; Kalichman et al., 2020; Liimatainen et al., 2020; Liimatainen et al., 2022). However, it is highly unfortunate to state that only 37 members of the Cortinariaceae family have been identified from the tropical, subtropical, and temperate regions of India, one of the megadiverse countries of the world (Bose et al., 2024a; Bose et al., 2024b; Bose et al., 2025). Species of the Cortinariaceae have a cosmopolitan distribution, ranging from tropical to arctic regions. They also form important ectomycorrhizal associations with many vascular plants from families like Pinaceae, Fagaceae, Dipterocarpaceae, Myrtaceae, Salicaceae, Fabaceae, Betulaceae, Nothofagaceae, Rosaceae, and others, providing access to nitrogen and aiding in carbon cycling (Acar, 2022; Liimatainen et al., 2022; Garnica et al., 2005). Members of this family should be investigated and documented scientifically because it possesses several strikingly important characteristics necessary for ecological sustainability. They serve as indicators of ecological fluctuations, such as changes caused by radioactive deposits, industrial air pollution, and acidification (Høiland & Jensen, 2000). Regarding their economic importance, they serve as potential delicacies. For example, *Thaxterogaster multiformis* (Fr.) Niskanen & Liimat. and *T. purpurascens* (Fr.) Niskanen & Liimat. are widely consumed in China (Dai et al., 2010). *Thaxterogaster turmalis* (Fr.) Niskanen & Liimat. has antitumor properties (Dai et al., 2008), while *Cortinarius infractus* (Pers.) Fr. contains two significant alkaloids, infractopicrin and 10-hydroxy-infractopicrin, used for potential cure of Alzheimer's disease (Geissler et al., 2010). *Cortinarius steglichii* N. Arnold, Palfner, Peintner & Huymann, reported from Chilean *Nothofagus* Forest, produces an important secondary metabolite namely, steglichon (a diterpenoid), which has antibacterial and anticancer activity (Lam et al., 2024). Additionally, certain species within this family have been utilized as commercial dyes. Nevertheless, many members are known to be highly toxic and may cause severe intoxication if

inadvertently ingested, including *Cortinarius orellanus* Fr. and *C. rubellus* Cooke (Høiland & Jensen, 2000). Based on the surveyed IUCN data, species of this family need to be conserved due to the severe threats they face leading to their extinction. For instance, *Calonarius meinhardii* (Bon) Niskanen & Liimat., *C. murellensis* (Cors. Gut., Ballarà, Cadiñanos, Palazón & Mahiques) Niskanen & Liimat., *C. osloensis* (Brandrud, T.S. Jeppesen & Frøslev) Niskanen & Liimat., *C. atrovirens* (Kalchbr.) Niskanen & Liimat., *Phlegmacium stjernegaardii* (Brandrud & Frøslev) Niskanen & Liimat., *Cortinarius phrygianus* Fr., *C. Nouhra* & Kuhar, and many others are at risk, with the list continuing to grow (<https://www.iucnredlist.org>).

Initially, Singer (1951) established *Thaxterogaster* as a sequestrate genus to accommodate taxa with *Cortinarius*-like spores but characterized by basidiomata with a reduced stipe and a basally exposed hymenium with a loculate to lamellate gleba (Peintner et al., 2002). Singer and Smith considered this genus as representatives of Gastromycetes (Singer & Smith, 1958). Later, Moser (1964) and Horak and Moser (1965) observed that *Thaxterogaster* and *Cortinarius* are closely related and stated that *Thaxterogaster* is polyphyletic due to links between species or groups of species of *Thaxterogaster* and different subgenera of *Cortinarius*. Based on recent studies on available species in this genus it is understood that morphologically, species of *Thaxterogaster* are characterized by the presence of small to large sized agaricoid (phlegmacioid, myxacioid) or sequestrate basidiomata exhibiting range of colours from white, ochraceous, greenish, brown to purple; lamellae adnate, adnexed or emarginate, when young appear white, pale grey, pale brown, green, purple or with a purplish tint; stipe cylindrical, clavate, rooting or bulbous, bulb rounded to marginate white, pale brown, purple, some species with greenish colours, in some species usually turning deeper purple when bruised (Liimatainen et al., 2022; Ghosh et al., 2023).

Earlier, the entire classification was solely based on both macro- and micro-morphological characterizations. Later on, with the aid of the sequences derived from nrDNA internal transcribed spacer (ITS), Peintner et al. (2001) showed that *Thaxterogaster* was nested within *Cortinarius*. As a result, *Thaxterogaster* was

synonymized with *Cortinarius* sensu lato (Peintner et al., 2002). Recently, Liimatainen et al. (2022) considered *Thaxterogaster* as an independent genus and divided it into six subgenera: *Thaxterogaster* Niskanen & Liimatainen, *Cretaces* Niskanen & Liimatainen, *Multiformes* Niskanen & Liimatainen, *Riederorum* Niskanen & Liimatainen, *Scauri* Niskanen & Liimatainen, and *Variiegati* Niskanen & Liimatainen. They recognized 23 sections: *Multiformes*, *Cremeolini* (both belonging to the subg. *Multiformes*); *Vibratiles*, *Microspirmi*, *Verniciori*, *Olorinati*, *Caustici* (all belonging to the subg. *Vibratiles*); *Thaxterogaster*, *Alboaggregati* (both belonging to the subg. *Thaxterogaster*); *Purpurascetes*, *Scauri* (both belonging to the subg. *Scauri*); *Rapacea*, *Gigasperma*, *Malvacei*, *Turmales*, *Pinophili*, *Austricyanites*, *Lustrati*, *Laquelli*, *Austrovaginati* (these nine sections are highly challenging and do not belong to any particular subgenus); *Cretaces* (belongs to the subg. *Cretaces*); *Riederorum* (belongs to the subg. *Riederorum*) and *Variiegati* (belongs to the subg. *Variiegati*) based on targeted capture sequencing and shallow whole genome sequencing (Liimatainen et al., 2022; Xie et al., 2023; Wang et al., 2025).

This is the second largest genus in Cortinariaceae, with nearly two hundred species worldwide and is currently considered to be a bihemispherical genus (Wang et al., 2025). In India, only five species of *Thaxterogaster* have been reported: *T. carneus* S.S. Ahmed & Z.A. Reshi, *T. indopurpurascens* (Dima, Semwal, Brandrud, V. Papp, & V.K. Bhatt) A. Ghosh, D. Chakr., K. Das & Vizzini, *T. purpurascens* (Fr.) Niskanen & Liimat., *T. shoreae* A. Ghosh, D. Chakr., K. Das & Vizzini and *T. thindii* A. Bose & D. Chakr (Bose et al., 2024a; Bose et al., 2025). As mentioned above, *Thaxterogaster* subgenus *Scauri* includes two sections: sect. *Scauri* and sect. *Purpurascetes* (Liimatainen et al., 2022). The species of sect. *Purpurascetes* are characterized by mostly stipitocarpic or few sequestrate basidiomata; hemispherical pilei; lamellae and stipe surfaces that usually turn deeper purple when bruised; and a positive iodine-based reaction (Saar et al., 2014; Soop et al., 2019; Liimatainen et al., 2014, 2022).

During a routine macrofungal survey conducted in the Tawang District of Arunachal Pradesh, India, several specimens from the genus *Thaxterogaster* were collected. After careful examination of both macro- and

micromorphological characteristics followed by molecular phylogenetic studies, our specimen was identified as *Thaxterogaster pallidopurpurascens* Zhu L. Yang & Zi R. Wang, a new record to India and was found to be a representative of the subgenus *Scauri*, sect. *Purpurascetes*. This study provides detailed macro- and micromorphological descriptions of this species, along with its nrITS-based molecular phylogenetic estimation.

## 2. MATERIALS AND METHODS

### 2.1 Morphological Studies

Thorough and extensive macrofungal explorations to the Tawang district of Arunachal Pradesh in general and near Sangestar Tso (commonly known as Madhuri Lake) in particular were undertaken during the rainy season of 2023 (July to August), which led to the collection of several fresh basidiomata belonging to Cortinariaceae. Macromorphological characters were recorded and analyzed from fresh basidiomata in the field. Photographs of the samples were taken both in the field and in the basecamp with the aid of Sony DSC-HX400V Cyber-shot camera. Color codes and terms were based on Kornerup and Wanscher (1978). After noting all the macromorphological characters, dissected samples were placed for drying in an aluminium field drier. Macro-chemical colour test was carried out with 5% KOH and 10% KOH solutions on surface of pileus and stipe of fresh basidiomata. Micromorphological characters were observed from free hand sections of dried materials mounted in a solution of 5% KOH, 1% Phloxin, and 1% ammoniacal Congo red with an Olympus CX 41 compound microscope. Drawings of the anatomical features were made with a drawing tube attached to Olympus CX 41 compound microscope at 1000x magnification. Micro-photographs were taken with a dedicated camera attached to an Olympus BX 53 microscope. Basidiospores were examined in Melzer's reagent and measured in side view, excluding ornamentations. Basidiospore measurements and length/width ratios (Q) are represented as: minimum–mean–maximum. Basidium length excludes the length of sterigmata. Forty (40) and twenty (20) measurements were taken for basidiospores and other micromorphological structures, respectively. The studied specimens were deposited in the Central National Herbarium (CAL), Howrah.

## 2.2 DNA Extraction, PCR Amplification and Sequencing

Following the manufacturer's instructions, 100 mg of dried mushroom samples were used to extract genomic DNA using the InstaGene™ 127 Matrix Genomic DNA isolation kit. The primers ITS1-F and ITS4 were used to amplify the ITS gene region (White et al., 1990; Gardes & Bruns, 1993). Initial denaturation at 94°C for 3 minutes, 35 cycles of denaturation at 94°C for 1 minute, annealing at 50°C for 30 seconds, and extension at 72°C for 1 minute comprised the PCR conditions. The ultimate extension was maintained for seven minutes at 72°C. The QIAquick PCR Purification Kit was then used to purify the PCR products. The amplifying primers are used in both xl DNA analyzers. Using Sequence Scanner, the obtained sequence's quality was examined. In this study, four sequences (two from each species) were generated from one species (*Thaxterogaster pallidopurpurascens*) and deposited in GenBank ([www.ncbi.nlm.nih.gov/genbank/](http://www.ncbi.nlm.nih.gov/genbank/)) (Table 1.). To edit the final tree, Inkscape ver. 0.92.4 was used.

## 2.3 Phylogenetic Analysis

The nrITS sequences of the newly recorded *Thaxterogaster pallidopurpurascens* and the top

BLASTn hits confirmed that our specimens belong to the genus *Thaxterogaster*. Species related to *T. pallidopurpurascens* were selected for phylogenetic analysis based on BLASTn results with >90% identity. Close relatives were sourced from GenBank (<https://www.ncbi.nlm.nih.gov/genbank>) and relevant published studies (Wang et al., 2025; Xie et al., 2023; Xie et al., 2024; Ghosh et al., 2023). A total of 66 taxa were included in the analysis, with *Thaxterogaster persicanus* (Soop) Niskanen & Liimat. used as the outgroup. The raw nrITS dataset was compiled independently. Sequence alignment was performed using the online version of the MAFFT v. 7 program (<https://mafft.cbrc.jp/alignment/software/>).

Phylogenetic analysis was carried out using the Maximum Likelihood (ML) inference method in IQ-TREE v2.4.0 (Nguyen et al., 2015), with TN+F+G4 (BIC) as the best-fitting model identified by ModelFinder (Kalyanamoorthy et al., 2017). An ultrafast bootstrap with 1000 replicates was applied to calculate nodal support values. Gaps in the alignment were treated as missing data during the phylogenetic analysis (Fig. 1). DNA sequences (Table 1) are deposited in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>).

**Table 1. A list of specimens and their corresponding voucher numbers and GenBank accession numbers used in this study**

Species name (as reported in GenBank)	Voucher/strain no.	Country	GenBank accession no. (nrITS)
<i>Cortinarius aff. purpurascens</i>	iNat14907654	USA	OK346437
<i>Thaxterogaster australis</i> Type	HO A20420A0	Australia	AY669615
<i>Thaxterogaster australis</i> Type	PDD:107712	New Zealand	KT875192
<i>Thaxterogaster atricapitatus</i>	KUN-HKAS 132012	China	PQ013314
<i>Thaxterogaster atricapitatus</i> Type	KUN-HKAS 82968	China	PQ013312
<i>Thaxterogaster cupreus</i>	KUN-HKAS 118275	China	PQ013316
<i>Thaxterogaster cupreus</i> Type	KUN-HKAS 117054	China	PQ013315
<i>Thaxterogaster collocandoides</i>	JAC12972	New Zealand	MW263688
<i>Thaxterogaster collocandoides</i> Type	PC:P. Moenne-Loccoz 5087	France	KF732287
<i>Thaxterogaster caesibulga</i> Type	KV660	Australia	GQ890310
<i>Thaxterogaster chlorophyllus</i>	PDD:103681	New Zealand	KF727375
<i>Thaxterogaster campbellae</i>	Trappe 19821	Australia	AF325558
<i>Thaxterogaster cinereoroseolus</i> Type	KV529	Australia	GQ890315
<i>Thaxterogaster cf. singularis</i>	PDD:103675	New Zealand	KF727376
<i>Thaxterogaster eumarginatus</i> Type	PC:A. Bidaud 07-10-175	France	NR_157935
<i>Thaxterogaster fuligineofolius</i> Type	IB910682	USA	NR_130219
<i>Thaxterogaster genuinus</i> Type	PC:X. Carteret 2005-132	France	NR_157937

Species name (as reported in GenBank)	Voucher/strain no.	Country	GenBank accession no. (nrITS)
<i>Thaxterogaster herpeticus</i>	TUB 019814	Europe	KJ421117
<i>Thaxterogaster herpeticus</i> Type	S:F44759	Sweden	NR_130224
<i>Thaxterogaster indopurpurascens</i> Type	KCS:2442	India	NR_173956
<i>Thaxterogaster indopurpurascens</i>	KCS2467	India	MW135431
<i>Thaxterogaster indopurpurascens</i>	KCS 2529	India	MW135430
<i>Thaxterogaster indopurpurascens</i>	AB001	India	PQ119953
<i>Thaxterogaster indopurpurascens</i>	AB002	India	PQ119958
<i>Thaxterogaster kaimanawa</i>	PDD:73133	New Zealand	JX000353
<i>Thaxterogaster kaimanawa</i>	PDD:101841	New Zealand	KJ635213
<i>Thaxterogaster largoides</i> Type	PC:P. Moenne-Loccoz 2336	France	NR_153011
<i>Thaxterogaster mutabilis</i> Type	MICH:10379	USA	KF732353
<i>Thaxterogaster montanus</i> Type	MICH:10377	USA	NR_130231
<i>Thaxterogaster occidentalis</i> Type	MICH:10382	USA	KF732357
<i>Thaxterogaster persicanus</i> Type	PDD:70507	New Zealand	NG_058791
<i>Thaxterogaster porphyropus</i> Type	S:F47381	Sweden	NR_130246
<i>Thaxterogaster porphyropus</i>	TN10-004	Canada	KF732513
<i>Thaxterogaster pallidopurpurascens</i>	KUN-HKAS 98034	China	PQ013325
<i>Thaxterogaster pallidopurpurascens</i> Type	KUN-HKAS 132009	China	PQ013324
<b><i>Thaxterogaster pallidopurpurascens</i></b>	<b>AP23-63</b>	<b>India</b>	<b>PP892258</b>
<b><i>Thaxterogaster pallidopurpurascens</i></b>	<b>AP23-64</b>	<b>India</b>	<b>PP892259</b>
<i>Thaxterogaster purpurascens</i>	-	Estonia	UDB016117
<i>Thaxterogaster purpurascens</i> Type	M:0275848	Spain	KT159218
<i>Thaxterogaster purpurascens</i>	M:0275852	Italy	KT159222
<i>Thaxterogaster purpurascens</i>	IK09-1510	Finland	KF732644
<i>Thaxterogaster purpurascens</i>	MQ19-CMMF001200	Canada	MN751459
<i>Thaxterogaster purpurascens</i>	SSMC OLY-AL0376	USA	OP941371
<i>Thaxterogaster purpurascens</i>	TUB 011401	Germany	AY174858
<i>Thaxterogaster purpurascens</i> Type	H:I. Kytovuori 98- 2121	Sweden	KF732406
<i>Thaxterogaster rhipiduranus</i> Type	PDD:88269	New Zealand	NR_157902
<i>Thaxterogaster rhipiduranus</i>	PDD:103673	New Zealand	KF727377
<i>Thaxterogaster rhodophyllus</i>	TUB 020416	-	KJ421051
<i>Thaxterogaster scaurus</i>	UBC-F17134- OC62	-	GQ159877
<i>Thaxterogaster sphagnophilus</i>	JFA13111	USA	FJ717592
<i>Thaxterogaster sordidus</i>	KUN-HKAS_135894	China	PQ013319
<i>Thaxterogaster sordidus</i> Type	KUN-HKAS_135896	China	PQ013318
<i>Thaxterogaster singularis</i> Type	PDD:78767	New Zealand	JQ287672
<i>Thaxterogaster submagellanicus</i> Type	HO A20518A1	Australia	AY669614
<i>Thaxterogaster subpurpurascens</i>	-	Sweden	UDB00736
<i>Thaxterogaster subpurpurascens</i> Type	H:K. Liimatainen & T. Niskanen 08-059	Finland	KF732449
<i>Thaxterogaster subpurpurascens</i>	14615	Italy	JF907905
<i>Thaxterogaster shoreae</i> Type	AGDC 21-04	India	OP473976
<i>Thaxterogaster shoreae</i>	AGJH-017	India	OP473978

Species name (as reported in GenBank)	Voucher/strain no.	Country	GenBank accession no. (nrITS)
<i>Thaxterogaster</i> sp.	K:001435623	USA	OQ382899
<i>Thaxterogaster</i> sp.	K:001435624	USA	OQ382900
<i>Thaxterogaster</i> sp.	K:001435598	Canada	OQ382902
<i>Thaxterogaster</i> sp.	K:001435599	Canada	OQ382903
<i>Thaxterogaster</i> sp.	K:001435625	USA	OQ382901
<i>Thaxterogaster violaceonitens</i>	TN00-661	Finland	KF732506
<i>Thaxterogaster violaceonitens</i>	TN06-170	Finland	KF732505

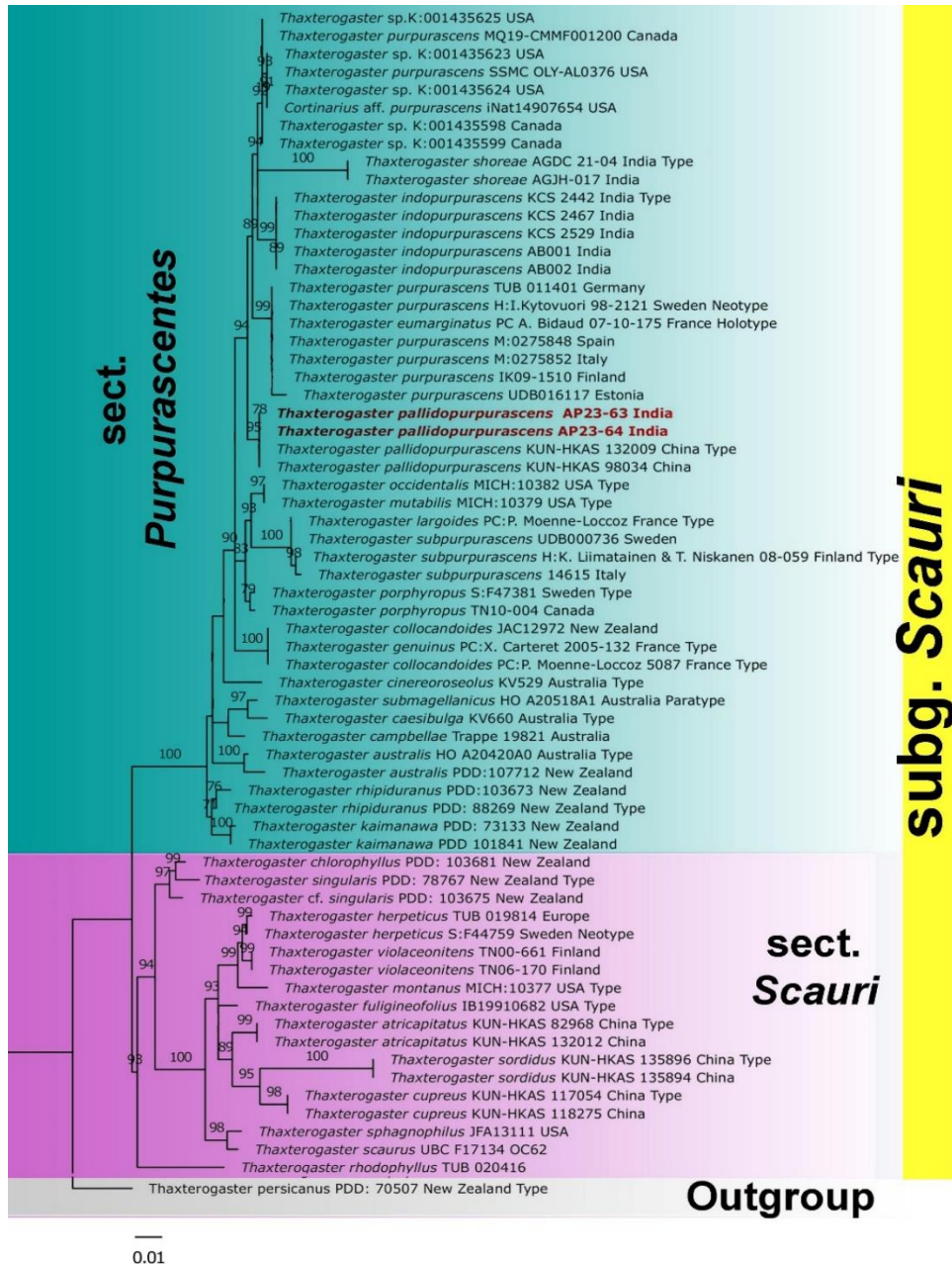


Fig. 1. Phylogram generated by maximum likelihood (ML) analysis based on ITS sequence data for *Thaxterogaster pallidopurpurascens* and allied species. Maximum likelihood bootstrap support values (MLBs)  $\geq 70\%$  are shown. This new record to India is highlighted in red to mark their phylogenetic positions in the tree

### 3. RESULTS AND DISCUSSION

#### 3.1 Phylogenetic Inferences

In our maximum likelihood (ML) phylogenetic analysis (Fig. 1), the nrITS data matrix included 66 taxa and 650 nucleotide positions (with gaps). The nrITS dataset consisted of 479 conserved sites, 161 variable sites, 121 parsimony-informative sites, 40 singleton sites, and 219 distinct patterns. The rate parameters were as follows: A-C: 1.00000, A-G: 3.02584, A-T: 1.00000, C-G: 1.00000, C-T: 5.18360, G-T: 1.00000. The base frequencies were A: 0.242, C: 0.201, G: 0.205, and T: 0.353.

Our Indian samples (GenBank accession numbers PP892258 and PP892259) grouped with *Thaxterogaster pallidopurpurascens*,

originally described from China (GenBank accession numbers PQ013324 and PQ013325), with strong support for this clade (ML bootstrap = 95%).

#### 3.2 Taxonomy

*Thaxterogaster pallidopurpurascens* Zhu L. Yang & Zi R. Wang (Wang et al. 2025) (Figs. 2–3).

Description: Pileus 40–70 mm in diam., convex when young; margin entire; surface moist and sticky when wet, greyish violet (17C4) near the margin, greyish brown to light brown (6D3–4) in the center, turning brown (6E7) with KOH. Lamellae adnate, crowded, greyish violet to dull violet (17B4–D4), turning purple (15B6–7) when bruised; lamellulae present in 3 series. Stipe 55–120 × 17–33 mm, sub-clavate to sub-bulbous,

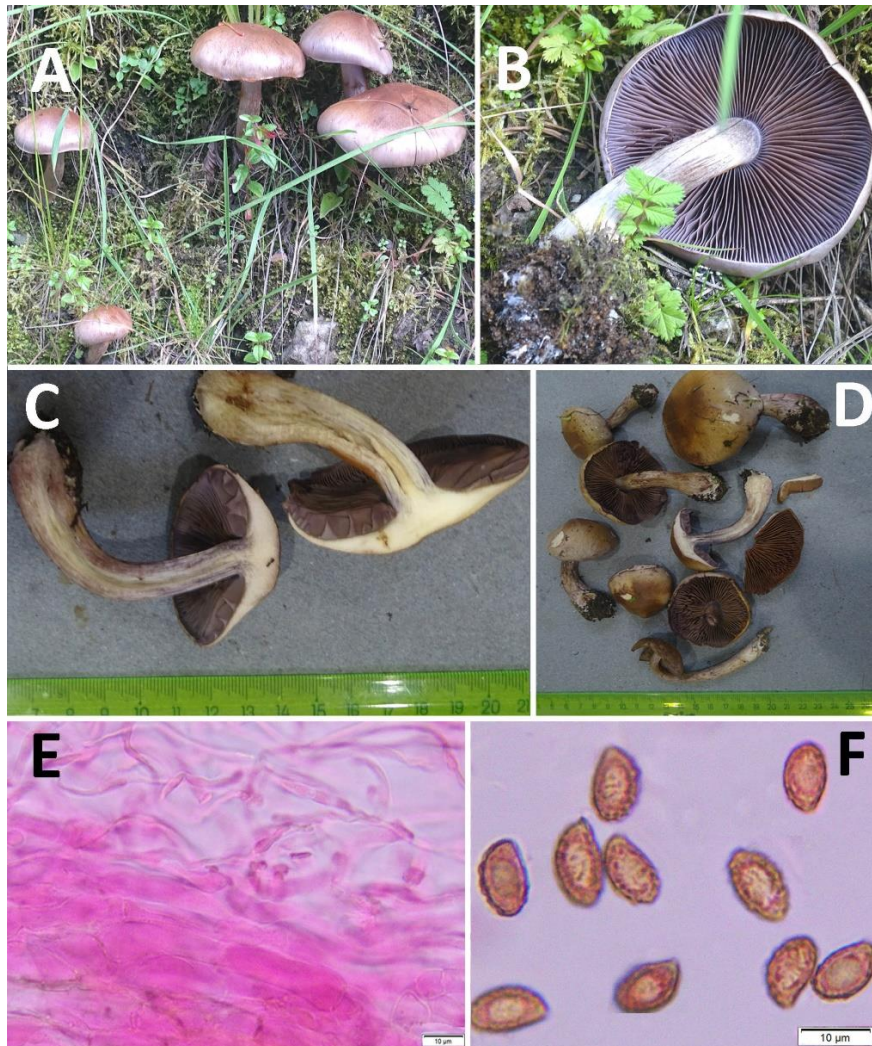
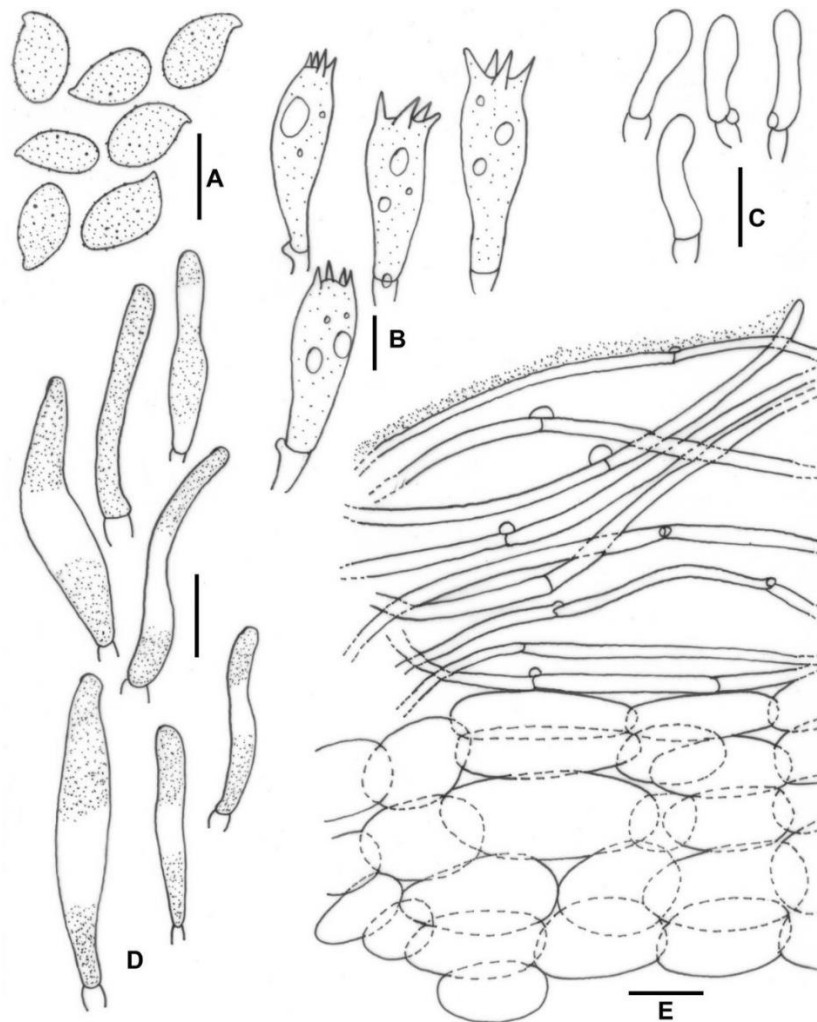


Fig. 2. *Thaxterogaster pallidopurpurascens*. (A–D) Fresh basidiomata, (E) transverse section through pileipellis of pileus, (F) basidiospores. Scale bars: E–F = 10 µm



**Fig. 3. *Thaxterogaster pallidopurpurascens*. (A) Basidiospores. (B) Basidia. (C) Sterile marginal elements. (D) Cheilocystidia. (E) Transverse section of pileipellis through pileus. Scale bars: A–E= 10  $\mu$ m**

slightly curved; surface violet-white (17A2) with white faint dark blond to pale violet (5D4–17C3) reticulation with fine fibrils and remnants of brownish universal veil of the mature basidiomata; base bulbous. Basal mycelium white. Pileus context solid and fleshy, grey (5B1) but changing to violet-white to pale violet (17A2–A3) after 10 minutes. Stipe context solid, grey (5B1) but changing to greyish violet (17B4–C4) after 10 minutes. Smell indistinct. Taste not recorded. Spore print rusty brown (6D7).

Basidiospores 9.4–12.50–15.3  $\times$  4.9–6.06–7.2  $\mu$ m (n= 40), Q= 1.51–1.71–2.17, oval to elliptical, moderately to strongly verrucose, dextrinoid. Basidia 40–49  $\times$  12–20  $\mu$ m, clavate, 4-spored; sterigmata triangular. Sterile marginal elements 16–18  $\times$  4–6  $\mu$ m, cylindrical to clavate, colourless and thin-walled. Cheilocystidia 28–45  $\times$  4.3–7.5

$\mu$ m, cylindrical to subcylindrical, occasionally present. Pileipellis 140–145  $\mu$ m thick, ixocutis, two-layered; suprapellis 56–62  $\mu$ m thick, made up of loosely interwoven somewhat parallel hyphae (55–61  $\times$  1.5–2.3  $\mu$ m); subpellis 85–92  $\mu$ m thick, consisting of slightly inflated, cylindrical, compactly arranged cells (36–53  $\times$  7.6–10.6  $\mu$ m). Clamp connections present in all tissues.

Specimen examined: INDIA. Arunachal Pradesh, Tawang district, Sangestar Tso, in temperate forest under *Rhododendron* sp., 17 Aug 2023, alt. 4297 m, N 27°42'46.20"E 91°53'37.95", Arvind Parihar, AP 23-63 (CAL 2007), GenBank no.: PP892258 and PP892259 (ITS).

Remarks: The presence of a sticky pileus with large basidiospores, along with ITS-based

phylogenetic analysis, places *T. pallidopurpurascens* in the subgenus *Scauri*, section *Purpurascentes*. The ITS sequence data, combined with morphological features such as ellipsoidal basidiospores, a greyish-brown central tint on the pileus, and a double-layered pileipellis with a thin glutinous surface layer, confirm that our Indian specimens belong to *T. pallidopurpurascens*, a species originally described from Yunnan, China (Wang et al. 2025). Although the macro- and micromorphological features mostly agree with the Chinese specimen, the latter has emarginate deep violet lamellae and lacks cheilocystidia (Wang et al., 2025).

Phylogenetically, *Thaxterogaster purpurascens* (Fr.) Niskanen & Liimat. (originally reported from Europe), is quite close to present Indian collections. However, *T. purpurascens* is separated by possessing a distinct marginate bulbous base, relatively paler pileus and smaller basidiospores (Saar et al., 2014; Ghosh et al., 2023; Xie et al., 2023; Xie et al., 2024; Wang et al., 2025).

#### 4. CONCLUSION

It is a grave reality that Cortinariaceae, the largest mushroom-producing family in the order Agaricales, is severely understudied in India. Despite its rich diversity of species, very little work is still being done worldwide, unlike the family Boletaceae Chevall., which also forms ectomycorrhizal associations with defined host trees (Sweta et al., 2025). This stands in contrast to other dominant ectomycorrhizal mushroom genera, such as *Russula* (1320 species worldwide, over 180 taxa in India), *Lactarius* (640 species worldwide, 83 taxa in India), *Amanita* (709 species worldwide, 65 species in India), and *Lactifluus* (178 species worldwide, 31 taxa in India), which are well-studied and scientifically identified in the country (Kalichman et al., 2020). As a result, much of the existing research is based on biased sampling. For instance, to establish an authentic and well-analyzed phylogenetic estimation of Indian Cortinariaceae species, we lack sufficient taxonomical and molecular data. Consequently, there remains a significant gap in studies on morphotaxonomy and molecular phylogeny within this family.

This genus is highly adaptable because its members can thrive in diverse habitats. As a result, morphological plasticity is a prominent

feature, even within the same species belonging to *Thaxterogaster* (Wang et al., 2025).

Most of the research on this genus has been conducted in Europe, North America, New Zealand, and Australia (Wang et al., 2025). However, to properly establish our Indian samples, we need verified data on Indian Cortinariaceae members. This data can be obtained from reliable sources such as GenBank (<https://www.ncbi.nlm.nih.gov/genbank>), the UNITE database (<https://unite.ut.ee>), Barcode of Life Database (BOLD) Systems (<https://www.boldsystems.org/>), Index Fungorum (<https://www.indexfungorum.org/>), and MycoBank (<https://www.mycobank.org/>). Therefore, the Cortinariaceae family should become a major area of focus in India in the coming years to address the gaps and enable unbiased future analyses of this family.

#### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

#### ACKNOWLEDGEMENT

We are grateful to the Director, Botanical Survey of India (BSI), Kolkata for providing all kinds of facilities to undertake the present research. We are also thankful to the Head of Office, BSI, Arunachal Pradesh Regional Centre, Itanagar and the Head of office, BSI, Central National Herbarium (CNH), Howrah for helping us in many ways. Entire Forest Department of Arunachal Pradesh is sincerely thanked for issuing survey permit to different forested areas of Arunachal Pradesh to one of us (AP). Help rendered by Dr. Sudeshna Datta, Botanist, CNH, BSI is duly acknowledged.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

- Acar, I. (2022). New records from Turkey: *Cortinarius barbatus*, *C. osmophorus*, & *C. saturninus*. *Mycotaxon*, 136(4), 819–830.
- Bose, A., Chakraborty, D., Datta, S., & Das, K. (2025). One new species of

- Thaxterogaster* subgenus *Riederorum* (Agaricales) from India. *International Journal of Plant & Soil Science*, 37, 180–187.  
<https://doi.org/10.9734/ijpss/2025/v37i25317>
- Bose, A., Niskanen, T., Datta, S., Ghosh, A., Vizzini, A., & Das, K. (2024a). Two new species and a new record of *Cortinarius* subgenus *Telamonia* (Agaricales) from India. *European Journal of Taxonomy*, 970, 38–60.  
<https://doi.org/10.5852/ejt.2024.970.2747>
- Bose, A., Uniyal, P., Vizzini, A., & Das, K. (2024b). Morphotaxonomy and molecular phylogeny unveil one new species and two new records of *Phlegmacium* (Cortinariaceae) from India. *Nordic Journal of Botany*, 2024, e04552.  
<https://doi.org/10.1111/njb.04552>
- Dai, Y.C., & Yang, Z.L. (2008). A revised checklist of medicinal fungi in China. *Mycosystema*, 27, 801–824.
- Dai, Y.C., Zhou, L.W., Yang, Z.L., Wen, H.A., Bau, T., & Li, T.H. (2010). A revised checklist of edible fungi in China. *Mycosystema*, 29, 1–21.
- Gardes, M., & Bruns, T.D. (1993). ITS primers with enhanced specificity for basidiomycetes—application to the identification of mycorrhizae and rusts. *Molecular Ecology*, 2, 113–118.  
<https://doi.org/10.1111/j.1365-294X.1993.tb00005.x>
- Garnica, S., Weiß, M., Oertel, B., & Franz, O. (2005). A framework for a phylogenetic classification in the genus *Cortinarius* (Basidiomycota, Agaricales) derived from morphological and molecular data. *Canadian Journal of Botany*, 83, 1457–1477.  
<https://doi.org/10.1139/b05-107>
- Geissler, T., Brandt, W., Porzel, A., Schlenzig, D., Kehlen, A., Wessjohann, L., & Arnold, N. (2010). Acetylcholinesterase inhibitors from the toadstool *Cortinarius infractus*. *Bioorganic & Medicinal Chemistry*, 18, 2173–2177.
- Ghosh, A., Chakraborty, D., Hembrom, M.E., Vizzini, A., & Das, K. (2023). *Thaxterogaster shoreae*, a new species of *Thaxterogaster* subg. *Scauri* sect. *Purpurascetes* from Sal Forest of India based on morphology and molecular phylogeny. *Taiwania*, 68(1), 23–30.  
<https://doi.org/10.6165/tai.2023.68.23>
- Høiland, K., & Holst-Jensen, A. (2000). *Cortinarius* phylogeny and possible taxonomic implications of ITS rDNA sequences. *Mycologia*, 92, 694–710.  
<https://doi.org/10.1080/00275514.2000.12061210>
- Kalichman, J., Kirk, P. M., & Matheny, P. B. (2020). A compendium of generic names of agarics and Agaricales. *Taxon*, 69, 425–447.  
<https://doi.org/10.1002/tax.12240>
- Kalyaanamoorthy, S., Minh, B.Q., Wong, T.K.F., Heaseler, A.V., & Jermini, L.S. (2017). ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods*, 14, 587–589.  
<https://doi.org/10.1038/nmeth.4285>
- Kornerup, A., & Wanscher, J. H. (1978). *Methuen handbook of colour* (3rd ed.). Eyre Methuen.
- Lam, Y.T., Schmitz, L., Huymann, L., Dhar, D., Morgan, I., Rennert, R., Davari, M.D., Peintner, U., Palfner, G., & Arnold, N. (2024). *Cortinarius steglichii*: A taxonomical and chemical novelty from Chile. *Mycological Progress*, 23, 55.  
<https://doi.org/10.1007/s11557-024-01983-z>
- Liimatainen, K., Kim, J. T., Pokorny, L., Kirk, P. M., Dentinger, B., & Niskanen, T. (2022). Taming the beast: A revised classification of *Cortinariaceae* based on genomic data. *Fungal Diversity*, 112, 89–170.  
<https://doi.org/10.1007/s13225-022-00499-9>
- Liimatainen, K., Niskanen, T., Dima, B., Ammirati, J. F., Kirk, P. M., & Kytövuori, I. (2020). Mission impossible completed: Unlocking the nomenclature of the largest and most complicated subgenus of *Cortinarius*, *Telamonia*. *Fungal Diversity*, 104, 291–331.  
<https://doi.org/10.1007/s13225-020-00459-1>
- Liimatainen, K., Niskanen, T., Dima, B., Kytövuori, I., Ammirati, J.F., & Frøslev, T.G. (2014). The largest type study of Agaricales species to date: Bringing identification and nomenclature of *Phlegmacium* (*Cortinarius*) into the DNA era. *Persoonia—Molecular Phylogeny and Evolution of Fungi*, 33, 98–140.  
<https://doi.org/10.3767/003158514X684681>
- Nguyen, L.T., Schmidt, H.A., Von Haeseler, A., & Minh, B.Q. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology Evolution*, 32, 268–274.  
<https://doi.org/10.1093/molbev/msu300>

- Peintner, U., Moser, M., & Vilgalys, R. (2002). *Thaxterogaster* is a taxonomic synonym of *Cortinarius*: New combinations and new names. *Mycotaxon*, 81, 177–184.
- Peintner, U., Moser, M.M., Thomas, K.A., & Manimohan, P. (2003). First records of ectomycorrhizal *Cortinarius* species (Agaricales, Basidiomycetes) from tropical India and their phylogenetic position based on rDNA ITS sequences. *Mycol. Res.*, 107, 485–494.
- Rajput, S., Chakraborty, D., Das, K., Ghosh, A., & Sharma, Y.P. (2025). First report of *Caloboletus panniformis* (Boletaceae) from India. *Indian Phytopathology*, 1–8. <https://doi.org/10.1007/s42360-025-00828-3>
- Saar, G., Dima, B., Schmidt-Stohn, G., Brandrud, T.E., Bellù, F., Frøslev, T.G., Oertel, B., & Soop, K. (2014). *Cortinarius* Untergattung *Phlegmacium* Sektion *Purpurascetes* in Europa. *Journal des J.E.C.*, 14, 140–161.
- Singer, R., & Smith, A.H. (1958). Studies on secotiaceae fungi—I: A monograph of the genus *Thaxterogaster*. *Brittonia*, 10, 201–216. <https://doi.org/10.2307/2804951>
- Soop, K., Dima, B., Cooper, J.A., Park, D., & Oertel, B. (2019). A phylogenetic approach to a global supraspecific taxonomy of *Cortinarius* (Agaricales) with an emphasis on the southern mycota. *Persoonia—Molecular Phylogeny and Evolution of Fungi*, 42, 261–290. <https://doi.org/10.3767/persoonia.2019.42.10>
- Wang, Z. R., Zhou, S. Y., Liu, F. F., & Yang, Z. L. (2025). The genus *Thaxterogaster* (Cortinariaceae): Phylogeny and species diversity in Western China. *Mycology*, 1–39. <https://doi.org/10.1080/21501203.2024.2441178>
- White, T.J., Bruns, T.D., Lee, S.B., & Taylor, J.W. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In M.A. Innis, D.H. Gelfand, J.J. Sninsky, & T.J. White (Eds.), *PCR Protocols: A Guide to Methods and Applications* (pp. 315–322). Academic Press.
- Xie, M.L., Feng, N., Lin, W.F., Su, W.Y., Li, Y., & Yang, Z.Q. (2023). Morphological and phylogenetic characterization of three novel *Thaxterogaster* (Cortinariaceae) species from China with an emphasis on their subtropical distribution. *Journal of Fungi*, 9, 1058. <https://doi.org/10.3390/jof9111058>
- Xie, M.L., Yu, Y., Long, P., Chen, Z.H., Wang, Z.R., Ma, H.X., Wei, T.Z., Liao, J.P., Li, C.T., Yang, Z.Q., & Li, Y. (2024). New insights into *Cortinarius*: Novel taxa from subtropical China. *Mycology*. <https://doi.org/10.1080/21501203.2024.2434584>

**Disclaimer/Publisher's Note:** The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of the publisher and/or the editor(s). This publisher and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

© Copyright (2025): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:  
The peer review history for this paper can be accessed here:  
<https://pr.sdiarticle5.com/review-history/134018>